



results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1108406271-19060-109558541338.BLASTQ4

Query=

(226 letters)

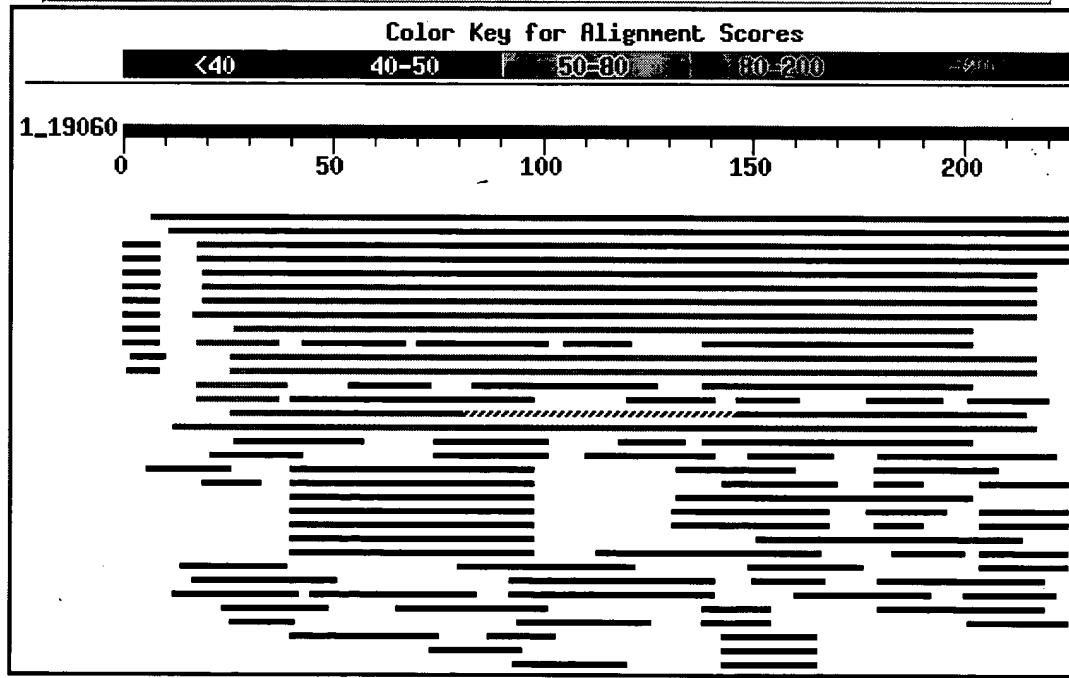
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,326,143 sequences; 788,882,796 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 101 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



[Related Structures](#)

Sequences producing significant alignments:

		Score (bits)	E Value
gi 505281 emb CAA41768.1	exoenzyme C3 [Clostridium botulinum]	630	e-179
gi 747707 emb CAA35828.1	exoenzyme C3 [Clostridium botulinum]	627	e-178
gi 51247865 pdb 1UZI B	Chain B, C3 Exoenzyme From Clostridium	609	e-173
gi 23200102 pdb 1GZE D	Chain D, Structure Of The Clostridium	599	e-170
gi 399048 sp Q00901 ARC3_CBCP	Mono-ADP-ribosyltransferase C...	338	2e-91
gi 56965901 pdb 1R4B B	Chain B, Adp-Ribosyltransferase C3bo...	338	2e-91
gi 404821 dbj BAA04492.1	ADP-ribosyltransferase C3 [Clostridium]	328	1e-88
gi 1212875 emb CAA60674.1	exoenzyme C3 [Clostridium limosum]	316	7e-85
gi 22795813 emb CAD22164.1	ADP-ribosyltransferase [Bacillus]	77	1e-12
gi 236587 gb AAB19984.1	ADP-ribosyltransferase exoenzyme C...	70	1e-10
gi 13186140 emb CAC33493.1	ADP-ribosyltransferase [Staphylococcus]	67	1e-09
gi 24636605 dbj BAC22946.1	epidermal cell differentiation	67	1e-09
gi 80491 pir S05236	exoenzyme C3 - Clostridium botulinum (...	62	4e-08
gi 236588 gb AAB19985.1	ADP-ribosyltransferase exoenzyme C...	60	2e-07
gi 17227179 ref NP_478345.1	hypothetical protein [Staphylococcus]	59	2e-07
gi 79857 pir JG0016	epidermal cell differentiation inhibitor	53	1e-05
gi 249591 gb AAB22208.1	ADP-ribosyltransferase [Clostridium]	41	0.089
gi 249592 gb AAB22209.1	ADP-ribosyltransferase [Clostridium]	40	0.12
gi 6730536 pdb 1QS1 D	Chain D, Crystal Structure Of Vegetativ...	40	0.12
gi 6730537 pdb 1QS2 A	Chain A, Crystal Structure Of Vip2 Wi...	40	0.12
gi 29650779 gb AAO86513.1	Vip2Ac [Bacillus thuringiensis]	40	0.16
gi 435823 gb AAB28629.1	C3-like ADP-ribosyltransferase [NA...	38	0.39
gi 45219853 gb AAH66784.1	Autoantigen La [Xenopus tropicalis]	38	0.52
gi 29374726 ref NP_813878.1	lipoprotein, putative [Enterococcus]	35	3.0
gi 15893630 ref NP_346979.1	Mono-ADP-ribosyltransferase C3...	35	3.0
gi 21315078 gb AAH30775.1	ARTS-1 protein [Homo sapiens] >g...	35	4.0
gi 37182302 gb AAQ88953.1	ARTS-1 [Homo sapiens]	35	4.0
gi 6642987 gb AAF20384.1	aminopeptidase PILS [Homo sapiens]	35	4.0
gi 6381989 gb AAF07395.1	adipocyte-derived leucine aminopeptidase	35	4.0
gi 19879276 gb AAK37778.1	adipocyte-derived leucine aminopeptidase	35	4.0
gi 23509168 ref NP_701836.1	hypothetical protein PFL2380c	35	4.0
gi 55625752 ref XP_527213.1	PREDICTED: similar to adipocyte-derived leucine aminopeptidase	35	4.0
gi 20137531 sp Q9NZ08 ART1_HUMAN	Adipocyte-derived leucine aminopeptidase	35	4.0
gi 20521069 dbj BAA25451.2	KIAA0525 protein [Homo sapiens]	35	4.0
gi 29655312 ref NP_821004.1	adenosylhomocysteinase [Coxiel]	35	5.4
gi 64876 emb CAA48716.1	La protein form B [Xenopus laevis]	34	7.3
gi 28436825 gb AAH46654.1	MGC52876 protein [Xenopus laevis]	34	7.3
gi 50083934 ref YP_045444.1	hypothetical protein; putative...	34	7.3
gi 2344808 emb CAB05387.1	unknown [Helicobacter pylori]	34	7.3
gi 18144707 dbj BAB80752.1	hypothetical protein [Clostridium]	34	7.3
gi 1006663 emb CAA84542.1	MDR3 P-glycoprotein [Homo sapiens]	34	9.8
gi 51473693 ref YP_067450.1	rickettsial conserved hypothetical protein	34	9.8
gi 48847109 ref ZP_00301367.1	COG0443: Molecular chaperone	34	9.8
gi 48844634 ref ZP_00298937.1	hypothetical protein Gmet020...	34	9.8
gi 48844300 ref ZP_00298619.1	COG0525: Valyl-tRNA synthetase	34	9.8
gi 48844054 ref ZP_00298396.1	COG2025: Electron transfer f...	34	9.8
gi 48843994 ref ZP_00298350.1	hypothetical protein Gmet020...	34	9.8
gi 34764189 ref ZP_00145051.1	TYPE I RESTRICTION-MODIFICAT...	34	9.8

gi 2313683 gb AAD07632.1 	H. pylori predicted coding region...	34	9.8	
gi 41723241 ref ZP_00150184.1 	COG0642: Signal transduction...	34	9.8	
gi 39594284 emb CAE71862.1 	Hypothetical protein CBG18908 [...]	34	9.8	
gi 39583135 emb CAE60675.1 	Hypothetical protein CBG04328 [...]	34	9.8	
gi 14276022 dbj BAB58942.1 	phenol hydroxylase large subuni...	34	9.8	
gi 730030 sp P40631 MLH_TETTH	Micronuclear linker histone p...	33	13	
gi 57208133 emb CAI40768.1 	Isp2a protein [Brevibacillus la...	33	13	
gi 51556700 ref YP_068061.1 	pTP [Tree shrew adenovirus]	33	13	
gi 27468972 ref NP_765609.1 	hypothetical protein SE2054 [S...	33	18	
gi 57865475 ref YP_189623.1 	membrane protein, putative [St...	33	18	
gi 53687109 ref ZP_00107385.2 	COG1177: ABC-type spermidine...	33	18	
gi 51013377 gb AAT92982.1 	YHR005C [Saccharomyces cerevisia...	32	24	
gi 173560 gb AAA18403.1 	putative. G-alpha-like protein	32	24	
gi 24377635 gb AAN58940.1 	conserved hypothetical protein; ...	32	24	
gi 7511574 pir T18747	probable potassium channel protein -...	32	24	
gi 48733274 ref ZP_00267017.1 	COG3451: Type IV secretory p...	32	32	
gi 30022154 ref NP_833785.1 	Stage V sporulation protein AD...	32	32	
gi 47529582 ref YP_020931.1 	stage v sporulation protein ad...	32	32	
gi 50906527 ref XP_464752.1 	putative pentatricopeptide (PP...	32	32	
gi 52141425 ref YP_085404.1 	stage V sporulation protein AD...	32	32	
gi 42783182 ref NP_980429.1 	stage V sporulation protein AD...	32	32	
gi 48870644 ref ZP_00323364.1 	COG3010: Putative N-acetylma...	32	32	
gi 48854717 ref ZP_00308878.1 	COG5651: PPE-repeat proteins...	32	32	
gi 47565952 ref ZP_00236991.1 	stage V sporulation protein ...	32	32	
gi 53687444 ref ZP_00108980.2 	COG4644: Transposase and ina...	32	32	
gi 39587376 emb CAE75030.1 	Hypothetical protein CBG22937 [...]	32	32	
gi 454862 gb AAA69970.1 	region near C-terminus; putative	32	32	
gi 16081318 ref NP_393636.1 	hypothetical protein Ta0158 [T...	32	43	
gi 54641100 gb EAL29851.1 	GA20157-PA [Drosophila pseudoobs...	32	43	
gi 52352362 gb AAU43652.1 	FAD/FMN-containing dehydrogenase...	32	43	
gi 15828932 ref NP_326292.1 	hypothetical protein MYPU_4610...	31	57	
gi 34104158 gb AAQ60517.1 	conserved hypothetical protein [...]	31	57	
gi 27467268 ref NP_763905.1 	penicillin amidase V [Staphylo...	31	57	
gi 49474859 ref YP_032900.1 	Adenosylhomocysteinase [Barton...	31	57	
gi 57168708 ref ZP_00367840.1 	conserved hypothetical prote...	31	57	
gi 41409460 ref NP_962296.1 	SahH [Mycobacterium avium subs...	31	57	
gi 29653858 ref NP_819550.1 	excinuclease ABC, B subunit [C...	31	57	
gi 52549567 gb AAU83416.1 	FAD FMN containing dehydrogenase...	31	57	
gi 30025120 gb AAC69093.2 	Innixin protein 5 [Caenorhabditi...	31	57	
gi 28828803 gb AAO51398.1 	hypothetical protein [Dictyostel...	31	57	
gi 50308841 ref XP_454425.1 	unnamed protein product [Kluyv...	31	57	
gi 48097538 ref XP_391917.1 	similar to CG11654-PA [Apis me...	31	57	
gi 57866161 ref YP_187823.1 	penicillin V acylase, putative...	31	57	
gi 17568579 ref NP_509403.1 	innixin, putative gap junction...	31	57	
gi 53735789 ref ZP_00178447.2 	hypothetical protein Cwat030...	31	57	
gi 46143226 ref ZP_00135639.2 	COG1404: Subtilisin-like ser...	31	57	
gi 39583806 emb CAE74879.1 	Hypothetical protein CBG22739 [...]	31	57	
gi 38491955 gb AAR22310.1 	mitochondrial intermediate pepti...	31	57	
gi 51534847 dbj BAD37204.1 	nitrite reductase [uncultured b...	31	57	
gi 236586 gb AAB19983.1 	ADP-ribosyltransferase exoenzyme C...	31	57	
gi 54020612 ref YP_116107.1 	DNA polymerase III alpha chain...	31	77	
gi 53729791 ref ZP_00150191.2 	COG2887: RecB family exonucl...	31	77	

Alignments

 [Get selected sequences](#) [Select all](#) [Deselect all](#)

>[gi|505281|emb|CAA41768.1|](#) exoenzyme C3 [Clostridium botulinum D phage]
[gi|296787|emb|CAA41767.1|](#) exoenzyme C3 [Clostridium botulinum C phage]
[gi|625586|pir||A38912](#) NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 prec
 Clostridium botulinum phage (strain CST)
[gi|399049|sp|P15879|ARC3 CBDP](#) Mono-ADP-ribosyltransferase C3 precursor (Exoenzyme
 Length = 251

Score = 630 bits (1479), Expect = e-179

Identities = 209/224 (93%), Positives = 210/224 (93%), Gaps = 7/224 (3%)

Query: 8 QACNAYSFNQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK 67
 Q C AYS NQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK

Sbjct: 30 QKCYAYSINQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK 89

Query: 68 LRQNKGVINGFPSNLIKQ--WLLDKSFNKMKT PENIMLF XGDDPAYLGTEFQNTLLNSNG 125
 LRQNKGVINGFPSNLIKQ LLDKSFNKMKT PENIMLF GDDPAYLGTEFQNTLLNSNG

Sbjct: 90 LRQNKGVINGFPSNLIKQVE-LLDKSFNKMKT PENIMLF RGDDPAYLGTEFQNTLLNSNG 148

Query: 126 TINKTAFEKAKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS 185
 TINKTAFEKAKA +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS

Sbjct: 149 TINKTAFEKAKA-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS 207

Query: 186 AFQGQLEG-LPRHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 AF GQLE LPRHSTYHIDDMRLSSDGKQIIITAT GTAINPK

Sbjct: 208 AFAGQLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 251

>[gi|747707|emb|CAA35828.1|](#) exoenzyme C3 [Clostridium botulinum D phage]
 Length = 218

Score = 627 bits (1472), Expect = e-178

Identities = 207/220 (94%), Positives = 208/220 (94%), Gaps = 7/220 (3%)

Query: 12 AYSFNQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN 71
 AYS NQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN

Sbjct: 1 AYSINQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN 60

Query: 72 KGVINGFPSNLIKQ--WLLDKSFNKMKT PENIMLF XGDDPAYLGTEFQNTLLNSNGTINK 129
 KGVINGFPSNLIKQ LLDKSFNKMKT PENIMLF GDDPAYLGTEFQNTLLNSNGTINK

Sbjct: 61 KGVINGFPSNLIKQVE-LLDKSFNKMKT PENIMLF RGDDPAYLGTEFQNTLLNSNGTINK 119

Query: 130 TAFEKAKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQG 189
 TAFEKAKA +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAF G

Sbjct: 120 TAFEKAKA-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAG 178

Query: 190 QLEG-LPRHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 QLE LPRHSTYHIDDMRLSSDGKQIIITAT GTAINPK

Sbjct: 179 QLEMMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 218

>gi|51247865|pdb|1UZI|B **S** Chain B, C3 Exoenzyme From Clostridium Botulinum, Tetr
 gi|51247864|pdb|1UZI|A **S** Chain A, C3 Exoenzyme From Clostridium Botulinum, Tetra
 gi|23200106|pdb|1GZF|D **S** Chain D, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|23200105|pdb|1GZF|C **S** Chain C, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|23200104|pdb|1GZF|B **S** Chain B, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|23200103|pdb|1GZF|A **S** Chain A, Structure Of The Clostridium Botulinum C3 Exoen
 (Wild-Type) In Complex With Nad
 gi|12084428|pdb|1G24|D **S** Chain D, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 gi|12084427|pdb|1G24|C **S** Chain C, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 gi|12084426|pdb|1G24|B **S** Chain B, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 gi|12084425|pdb|1G24|A **S** Chain A, The Crystal Structure Of Exoenzyme C3 From Clos
 Botulinum
 Length = 211

Score = 609 bits (1429), Expect = e-173

Identities = 201/213 (94%), Positives = 202/213 (94%), Gaps = 7/213 (3%)

Query: 19 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 78
 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF

Sbjct: 1 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 60

Query: 79 PSNLIKQ--WLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 136
 PSNLIKQ LLDKSFNKMKTPEINIMLF GDDPAYLGTEFQNTLLNSNGTINKTAFEKAK

Sbjct: 61 PSNLIKQVE--LLDKSFNKMKTPEINIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 119

Query: 137 AIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQQLEGP 195
 A +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAF GQLE LP

Sbjct: 120 A-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLP 178

Query: 196 RHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 RHSTYHIDDMRLSSDGKQIIITAT GTAINPK

Sbjct: 179 RHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 211

>gi|23200102|pdb|1GZE|D **S** Chain D, Structure Of The Clostridium Botulinum C3 Exo
 Mutant)
 gi|23200101|pdb|1GZE|C **S** Chain C, Structure Of The Clostridium Botulinum C3 Exoen
 Mutant)
 gi|23200100|pdb|1GZE|B **S** Chain B, Structure Of The Clostridium Botulinum C3 Exoen
 Mutant)
 gi|23200099|pdb|1GZE|A **S** Chain A, Structure Of The Clostridium Botulinum C3 Exoen
 Mutant)
 Length = 211

Score = 599 bits (1407), Expect = e-170

Identities = 200/213 (93%), Positives = 201/213 (94%), Gaps = 7/213 (3%)

Query: 19 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 78
 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF
 Sbjct: 1 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 60

Query: 79 PSNLIKQ--WLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 136
 PSNLIKQ LLDKSFNKMKT PENIMLF GDDPAYLGTEFQNTLLNSNGTINKTAFEKAK
 Sbjct: 61 PSNLIKQVE-LLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 119

Query: 137 AIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG-LP 195
 A +FLN DRLEYGYISTS MNVSQFAGRPIITKFKVAKGSKAGYIDPISAF GQLE LP
 Sbjct: 120 A-KFLNKDRLEYGYISTSCMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLP 178

Query: 196 RHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 RHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 179 RHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 211

>[gi|399048|sp|Q00901|ARC3_CBCP](#) Mono-ADP-ribosyltransferase C3 precursor (Exoenzy
[gi|80492|pir|A41021](#) NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 precu
 Clostridium botulinum phage (strain C003-9)
[gi|144737|gb|AAA23212.1|](#) C3 ADP-ribosyltransferase
 Length = 244

Score = 338 bits (791), Expect = 2e-91
 Identities = 129/205 (62%), Positives = 163/205 (79%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
 Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG P
 Sbjct: 42 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLP 101

Query: 80 SNL---IKQWLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
 +++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTINKT FE K
 Sbjct: 102 ADILQKVK--LIDQSFSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINKTVFEQVK 159

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
 AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
 Sbjct: 160 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFVKTNGSKGGYIDPISYFPQLEVL 215

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
 LPR+++Y+I DM++S + +QI+ITA
 Sbjct: 216 LPRNNNSYYISDMQISPNNRQIMITA 240

>[gi|56965901|pdb|1R4B|B](#) **S** Chain B, Adp-Ribosyltransferase C3bot2 From Clostridiu
 Monoclinic Form
[gi|56965900|pdb|1R4B|A](#) **S** Chain A, Adp-Ribosyltransferase C3bot2 From Clostridium
 Monoclinic Form
[gi|56965899|pdb|1R45|D](#) **S** Chain D, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form
[gi|56965898|pdb|1R45|C](#) **S** Chain C, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form
[gi|56965897|pdb|1R45|B](#) **S** Chain B, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form
[gi|56965896|pdb|1R45|A](#) **S** Chain A, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form
 Length = 204

Score = 338 bits (791), Expect = 2e-91
 Identities = 129/205 (62%), Positives = 163/205 (79%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
 Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG P
 Sbjct: 2 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLP 61

Query: 80 SNL---IKQWLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
 +++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTINKT FE K
 Sbjct: 62 ADILQKVK--LIDQSF SKM KMPQNIILFRGDDPAYLGPEFQDKILNKDGTINKTVFEQVK 119

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
 AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
 Sbjct: 120 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFVKTNGSKGGYIDPISYFPQLEVL 175

Query: 194 LPRHSTYHIDMRLSSDGKQIIITA 218
 LPR+++Y+I DM++S + +QI+ITA
 Sbjct: 176 LPRNNNSYYISDMQISPNNRQIMITA 200

>gi|404821|dbj|BAA04492.1| ADP-ribosyltransferase C3 [Clostridium botulinum D]
 Length = 244

Score = 328 bits (768), Expect = 1e-88
 Identities = 127/205 (61%), Positives = 161/205 (78%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
 Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG
 Sbjct: 42 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLS 101

Query: 80 SNL---IKQWLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
 S++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTIN+ FE K
 Sbjct: 102 SDILQKVK--LIDQSF SKM KMPQNIILFRGDDPAYLGPEFQDKILNKDGTINRDVFEQVK 159

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
 AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
 Sbjct: 160 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFVKTNGSKGGYIDPISYFPQLEVL 215

Query: 194 LPRHSTYHIDMRLSSDGKQIIITA 218
 LPR+++Y+I DM++S + +QI+ITA
 Sbjct: 216 LPRNNNSYYISDMQISPNNRQIMITA 240

>gi|1212875|emb|CAA60674.1| exoenzyme C3 [Clostridium limosum]
 gi|2498151|sp|Q46134|ARC3_CLOLM Mono-ADP-ribosyltransferase C3 precursor (Exoenzyme C3-
 precursor [validated] - Clostridium limosum phage
 Length = 250

Score = 316 bits (739), Expect = 7e-85
 Identities = 126/205 (61%), Positives = 160/205 (78%), Gaps = 7/205 (3%)

Query: 18 KAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVING 77
 K Y+++++EFTNID+A+AWG+ Q+ KY LS SEK A+ YT++A+ ING LR N+G NG
 Sbjct: 45 KPYADSFKEFTNIDEARAWGDKQFAKYKLSSEKNALTIYTRNAARINGPLRANQGNTNG 104

Query: 78 FPSNLIK---QWLLDKSFNKMKTPENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEK 134
 P+++ K Q +DKSF KM+TPENI+LF GDDP YLG +F+NT+LN +GTINK FE+
 Sbjct: 105 LPADIRKEVEQ--IDKSFTKMOTPENIILFRGDDPGYLGPDFENTILNRDTINKAVFEQ 162

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
 K ++F DR EGYISTSL+N S FAGRPIITKFKV GSKAGYI+PIS F+GQLE
 Sbjct: 163 VK-LRFKGKDRKEYGYISTSLVNGSAFAGRPIITKFKVLDGSKAGYIEPISTFKGQLEVL 221

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
 LPR STY I DM+++ + KQIIITA
 Sbjct: 222 LPRSSTYTISDMQIAPNNKQIIITA 246

>gi|22795813|emb|CAD22164.1| ADP-ribosyltransferase [Bacillus cereus]
 Length = 219

Score = 76.6 bits (173), Expect = 1e-12
 Identities = 74/209 (35%), Positives = 108/209 (51%), Gaps = 64/209 (30%)

Query: 28 TNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEIN-----GKL-----RQNKGVI 75
 TN ++A AWG Q+ K+ SK EK AI YTK+A N GKL + K I
 Sbjct: 20 TNKEEADAWGKKQFNKW--SKEEKAIRDYTKNARPYNEFLRMHAGKLDSDPTMKKK--I 75

Query: 76 NGFPSNLIKQWLDKSFNKM--KTPENIMLFXGDDPAYL-GTEFQNTLLNSNGTINKTAF 132
 LDK+ N+ K +NI ++ GDD A++ G E+ N+++ NG +++
 Sbjct: 76 ES-----LDKALNRKEAKVNDNIKVYRGDD-AWIFGKEYDNSIIK-NGKVDR--- 120

Query: 133 EKAKAIQ--FLNXDRL-----EYGYISTS-LMNVSQFAG---RPIITKFKVAKGSKAG 179
 EK K IQ F E+GYISTS L++ AG RP++T+FKV G+
 Sbjct: 121 EKFKEIQKKF-----QGKTTTEFGYISTSILID---AGYAKTRPVMTEFKVGSGTHGA 170

Query: 180 YI--DPISAFQGQ---LEGLPRHSTYHID 203
 Y+ D ++A+ GQ L LPR++ Y I+
 Sbjct: 171 YMNSDDLTAYPGQYELL--LPRNTVYKIE 197

>gi|236587|gb|AAB19984.1| ADP-ribosyltransferase exoenzyme C3 [Clostridium botulinum C strain Stockholm, CST, Peptide Partial, 20 aa]
 Length = 20

Score = 69.8 bits (157), Expect = 1e-10
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 19 AYSNTYQEFTNIDQAKAWGN 38
 AYSNTYQEFTNIDQAKAWGN
 Sbjct: 1 AYSNTYQEFTNIDQAKAWGN 20

>gi|13186140|emb|CAC33493.1| ADP-ribosyltransferase [Staphylococcus aureus]
gi|34810145|pdb|1OJZ|A **S** Chain A, The Crystal Structure Of C3stau2 From S. Aureus
 Nad
gi|34810144|pdb|1OJQ|A **S** Chain A, The Crystal Structure Of C3stau2 From S. Aureus
 Length = 212

Score = 66.8 bits (150), Expect = 1e-09

RID=1108406271-19060-109558541338.BLASTQ4,

Identities = 78/232 (33%), Positives = 113/232 (48%), Gaps = 70/232 (30%)

Query: 27 FTNIDQAKAWGNAQYK--KYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNL-- 82
FT++ +A WGN+ K KY SK +K AI +YTK++S IN LR G +N N+
Sbjct: 6 FTDLVEATKWGNSLIKSAKYS-SK-DKMAIYNYTKNSSPINTPLRSANGDVNKLENIQE 63

Query: 83 -IKQWLLDKSFNKMKTPENI---MLFXGDDPAYLG--TEF-----Q---- 117
++Q LD + +K TP++ +L + YL T F Q
Sbjct: 64 QVRQ--LDSTISKSVTPDSVYVYRLL---NLDYLSITGFTREDLHMLQQTNNGQYNEA 117

Query: 118 -----NTLLNSNGTINKTAFEKAKAIQFLNXDRL--EYGYISTSLMNVSQFAGRPIITKF 170
N L+NS R+ E GY ST L++ + AGRPI K
Sbjct: 118 LVSKLNNLMNS-----RIYRENGYSSTQLVSGAALAGRPIELKL 156

Query: 171 KVAKGSKAGYIDP--ISAFQGQLEG-LPRHSTYHIDDMRLSSDGKQ-IIITA 218
++ KG+KA YID ++A+ GQ E LPR + Y + ++L SD K+ IIITA
Sbjct: 157 ELPKGTKAAYIDSKELTAYPGQQEVLLPRGTEYAVGSVKL-SDNKRKIIITA 207

>gi|24636605|dbj|BAC22946.1| epidermal cell differentiation inhibitor B [Staphylococcus aureus]
Length = 247

Score = 66.8 bits (150), Expect = 1e-09

Identities = 78/232 (33%), Positives = 113/232 (48%), Gaps = 70/232 (30%)

Query: 27 FTNIDQAKAWGNAQYK--KYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNL-- 82
FT++ +A WGN+ K KY SK +K AI +YTK++S IN LR G +N N+
Sbjct: 41 FTDLVEATKWGNSLIKSAKYS-SK-DKMAIYNYTKNSSPINTPLRSANGDVNKLENIQE 98

Query: 83 -IKQWLLDKSFNKMKTPENI---MLFXGDDPAYLG--TEF-----Q---- 117
++Q LD + +K TP++ +L + YL T F Q
Sbjct: 99 QVRQ--LDSTISKSVTPDSVYVYRLL---NLDYLSITGFTREDLHMLQQTNNGQYDEA 152

Query: 118 -----NTLLNSNGTINKTAFEKAKAIQFLNXDRL--EYGYISTSLMNVSQFAGRPIITKF 170
N L+NS R+ E GY ST L++ + AGRPI K
Sbjct: 153 LVSKLNNLMNS-----RIYRENGYSSTQLVSGAALAGRPIELKL 191

Query: 171 KVAKGSKAGYIDP--ISAFQGQLEG-LPRHSTYHIDDMRLSSDGKQ-IIITA 218
++ KG+KA YID ++A+ GQ E LPR + Y + ++L SD K+ IIITA
Sbjct: 192 ELPKGTKAAYIDSKELTAYPGQQEVLLPRGTEYAVGSVKL-SDNKRKIIITA 242

>gi|80491|pir||S05236| exoenzyme C3 - Clostridium botulinum (fragment)
Length = 22

Score = 61.7 bits (138), Expect = 4e-08

Identities = 21/23 (91%), Positives = 21/23 (91%), Gaps = 2/23 (8%)

Query: 19 AYSNTYQEF-TNIDQAKAWGNAQ 40
AYSN TYQEF TNIDQAKA GNAQ
Sbjct: 1 AYSNTYQEFNTNIDQAKA-GNAQ 22

>gi|236588|gb|AAB19985.1| ADP-ribosyltransferase exoenzyme C3 [Clostridium botulinum D strain D1873, Peptide Partial, 20 aa]
Length = 20

Score = 59.6 bits (133), Expect = 2e-07
 Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 19 AYSNTYQEFTNIDQAKAWGN 38
 AYSNTYQEFTNIDQAKA GN
 Sbjct: 1 AYSNTYQEFTNIDQAKAXGN 20

□>gi|17227179|ref|NP_478345.1| hypothetical protein [Staphylococcus aureus]
gi|17148579|dbj|BAB78400.1| ORF2~epidermal cell differentiation inhibitor C of St
 aureus
 Length = 247

Score = 59.2 bits (132), Expect = 2e-07
 Identities = 35/75 (46%), Positives = 49/75 (65%), Gaps = 7/75 (9%)

Query: 147 EYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDP--ISAFQGQ---LEGLPRHSTYH 201
 EYGY ST L+ + AGRPI K ++ KG+KA YID ++A+ GQ L LPR + Y
 Sbjct: 168 EYGYSSSQLVKGAALAGRPIELKLQLPKGTAAAYIDSKNLTAYPGQQEIL--LPRGTDYT 225

Query: 202 IDDMRLSSDGKQIII 216
 I+ ++LS D K+I+I
 Sbjct: 226 INTVKLSDDHKRILI 240

Score = 43.9 bits (96), Expect = 0.008
 Identities = 26/61 (42%), Positives = 37/61 (60%), Gaps = 10/61 (16%)

Query: 27 FTNIDQAKAWGN----AQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSN 81
 FT++ +A WGN A Y SK +KEAI +YTK +S IN LR ++G I+ F ++
 Sbjct: 41 FTDLTEATNWGNKLIKQANYS---SK-DKEAIYNYTKYSSPINTPLRSSQGDISNFSAD 95

Query: 82 L 82
 L
 Sbjct: 96 L 96

□>gi|79857|pir||JG0016 epidermal cell differentiation inhibitor precursor - Staph
 aureus
gi|119131|sp|P24121|EDIN_STAAU Epidermal cell differentiation inhibitor precursor
gi|152998|gb|AAA26616.1| epidermal cell differentiation inhibitor
 Length = 247

Score = 53.2 bits (118), Expect = 1e-05
 Identities = 89/261 (34%), Positives = 119/261 (45%), Gaps = 93/261 (35%)

Query: 13 YSFNQK--AYSNTY----QEFTNIDQAKAWGNAQYK----KYGLSKSEKEAIVSYTKS 60
 YS N K SNT + FT++D+A WGN K KY S +K A+ YTK
 Sbjct: 20 YSINDKIIIEVSNTSLAADVKNFTDLDEATKWGN--KLIKQAKY--SSDDKIALYEYTKD 74

Query: 61 ASEINGKLRQNKGVINGFPSNLIKQWL-----LDKSFNKMKTPENI---ML--- 103
 +S+ING LR G IN K L LD S +K TPE++ +L
 Sbjct: 75 SSKINGPLRLAGGDIN-----K--LDSTTQDKVRRLDSSISKSTTPESVYVYRLLNLD 125

Query: 104 -----FXGDDPAY-LGTEFQNTLLNSNGTINKTAFEKAKAIQF-----LN---XDR 145